FrÃ©dÃ©ric Choulet

List of Publications by Year
in descending order

48 papers	9,120 citations	159585 30 h-index	197818 49 g-index
54 all docs	54 docs citations	54 times ranked	7336 citing authors

#	Article	IF	Citations
1	Long-read and chromosome-scale assembly of the hexaploid wheat genome achieves high resolution for research and breeding. GigaScience, 2022, 11, .	6.4	26
2	New insights into homoeologous copy number variations in the hexaploid wheat genome. Plant Genome, 2021, 14, e20069.	2.8	16
3	Optical maps refine the bread wheat Triticum aestivum cv. Chinese Spring genome assembly. Plant Journal, 2021, 107, 303-314.	5.7	237
4	Structural Variations Affecting Genes and Transposable Elements of Chromosome 3B in Wheats. Frontiers in Genetics, 2020, 11, 891.	2.3	16
5	Deciphering carbohydrate metabolism during wheat grain development via integrated transcriptome and proteome dynamics. Molecular Biology Reports, 2020, 47, 5439-5449.	2.3	15
6	Worldwide phylogeography and history of wheat genetic diversity. Science Advances, 2019, 5, eaav0536.	10.3	118
7	Identification, Molecular Cloning, and Functional Characterization of a Wheat UDP-Glucosyltransferase Involved in Resistance to Fusarium Head Blight and to Mycotoxin Accumulation. Frontiers in Plant Science, 2018, 9, 1853.	3.6	22
8	Annotation, classification, genomic organization and expression of the Vitis vinifera CYPome. PLoS ONE, 2018, 13, e0199902.	2.5	11
9	Optical and physical mapping with local finishing enables megabase-scale resolution of agronomically important regions in the wheat genome. Genome Biology, 2018, 19, 112.	8.8	41
10	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
11	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
12	Impact of transposable elements on genome structure and evolution in bread wheat. Genome Biology, 2018, 19, 103.	8.8	226
13	Linking the International Wheat Genome Sequencing Consortium bread wheat reference genome sequence to wheat genetic and phenomic data. Genome Biology, 2018, 19, 111.	8.8	232
14	High throughput SNP discovery and genotyping in hexaploid wheat. PLoS ONE, 2018, 13, e0186329.	2.5	200
15	High-Resolution Mapping of Crossover Events in the Hexaploid Wheat Genome Suggests a Universal Recombination Mechanism. Genetics, 2017, 206, 1373-1388.	2.9	72
16	Exploiting the Repetitive Fraction of the Wheat Genome for Highâ€Throughput Singleâ€Nucleotide Polymorphism Discovery and Genotyping. Plant Genome, 2016, 9, plantgenome2015.09.0078.	2.8	13
17	Major Gene for Field Stem Rust Resistance Co-Locates with Resistance Gene Sr12 in â€˜Thatcherâ€™ Wheat. PLoS ONE, 2016, 11, e0157029.	2.5	37
18	De Novo Annotation of Transposable Elements: Tackling the Fat Genome Issue. Proceedings of the IEEE, 2016, , 1-8.	21.3	8

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19	Fine mapping of a large-effect QTL conferring Fusarium crown rot resistance on the long arm of chromosome 3B in hexaploid wheat. BMC Genomics, 2015, 16, 850.	2.8	40
20	Deep transcriptome sequencing provides new insights into the structural and functional organization of the wheat genome. Genome Biology, 2015, 16, 29.	8.8	101
21	Small-scale gene duplications played a major role in the recent evolution of wheat chromosome 3B. Genome Biology, 2015, 16, 188.	8.8	76
22	Organization and evolution of transposable elements along the bread wheat chromosome 3B. Genome Biology, 2014, 15, 546.	8.8	88
23	QTug.sau-3B Is a Major Quantitative Trait Locus for Wheat Hexaploidization. G3: Genes, Genomes, Genetics, 2014, 4, 1943-1953.	1.8	26
24	High-resolution analysis of a QTL for resistance to Stagonospora nodorum glume blotch in wheat reveals presence of two distinct resistance loci in the target interval. Theoretical and Applied Genetics, 2014, 127, 573-586.	3.6	11
25	Genotyping by sequencing transcriptomes in an evolutionary pre-breeding durum wheat population. Molecular Breeding, 2014, 34, 1531-1548.	2.1	20
26	Meiotic Gene Evolution: Can You Teach a New Dog New Tricks?. Molecular Biology and Evolution, 2014, 31, 1724-1727.	8.9	71
27	A chromosome-based draft sequence of the hexaploid bread wheat (Triticum aestivum) genome. Science, 2014, 345, 1251788.	12.6	1,479
28	Structural and functional partitioning of bread wheat chromosome 3B. Science, 2014, 345, 1249721.	12.6	542
29	Ancient hybridizations among the ancestral genomes of bread wheat. Science, 2014, 345, 1250092.	12.6	629
30	Transcriptome and Allele Specificity Associated with a 3BL Locus for Fusarium Crown Rot Resistance in Bread Wheat. PLoS ONE, 2014, 9, e113309.	2.5	42
31	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. Genome Biology, 2013, 14, R64.	8.8	45
32	Wheat centromeric retrotransposons: the new ones take a major role in centromeric structure. Plant Journal, 2013, 73, 952-965.	5.7	78
33	dbWFA: a web-based database for functional annotation of Triticum aestivum transcripts. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat014.	3.0	9
34	Genome-level identification of cell wall invertase genes in wheat for the study of drought tolerance. Functional Plant Biology, 2012, 39, 569.	2.1	18
35	Whole Genome Profiling provides a robust framework for physical mapping and sequencing in the highly complex and repetitive wheat genome. BMC Genomics, 2012, 13, 47.	2.8	29
36	Intraspecific sequence comparisons reveal similar rates of non-collinear gene insertion in the B and D genomes of bread wheat. BMC Plant Biology, 2012, 12, 155.	3.6	18

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37	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. Frontiers in Plant Science, 2012, 3, 5.	3.6	73
38	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives Â. Plant Cell, 2011, 23, 1706-1718.	6.6	190
39	Variation in crossover rates across a 3-Mb contig of bread wheat (Triticum aestivum) reveals the presence of a meiotic recombination hotspot. Chromosoma, 2011, 120, 185-198.	2.2	55
40	A 3,000-Loci Transcription Map of Chromosome 3B Unravels the Structural and Functional Features of Gene Islands in Hexaploid Wheat Â. Plant Physiology, 2011, 157, 1596-1608.	4.8	49
41	Genetic diversity and linkage disequilibrium studies on a 3.1-Mb genomic region of chromosome 3B in European and Asian bread wheat (Triticum aestivum L.) populations. Theoretical and Applied Genetics, 2010, 121, 1209-1225.	3.6	11
42	Specific patterns of gene space organisation revealed in wheat by using the combination of barley and wheat genomic resources. BMC Genomics, 2010, 11, 714.	2.8	21
43	Insertion siteâ€based polymorphism markers open new perspectives for genome saturation and markerâ€assisted selection in wheat. Plant Biotechnology Journal, 2010, 8, 196-210.	8.3	111
44	Megabase Level Sequencing Reveals Contrasted Organization and Evolution Patterns of the Wheat Gene and Transposable Element Spaces. Plant Cell, 2010, 22, 1686-1701.	6.6	258
45	Conjugative Transfer of the Integrative Conjugative Elements ICESt1 and ICESt3 from Streptococcus thermophilus. Journal of Bacteriology, 2009, 191, 2764-2775.	2.2	55
46	A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. Science, 2008, 322, 101-104.	12.6	356
47	Intraspecific Variability of the Terminal Inverted Repeats of the Linear Chromosome of Streptomyces ambofaciens. Journal of Bacteriology, 2006, 188, 6599-6610.	2.2	32
48	Evolution of the Terminal Regions of the Streptomyces Linear Chromosome. Molecular Biology and Evolution, 2006, 23, 2361-2369.	8.9	96